

no extr. listed  
in PALM

1647

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/626,616

DATE: 12/01/2000  
TIME: 04:03:29

INPUT SET: S36161.raw

RECEIVED

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

DEC 05 2000

TECH CENTER 1600/2909

ENTERED #4

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Yu, Lei  
6  
7 (ii) TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
8  
9 (iii) NUMBER OF SEQUENCES: 17  
10  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: Arnold, White & Durkee  
13 (B) STREET: P. O. Box 4433  
14 (C) CITY: Houston  
15 (D) STATE: TX  
16 (E) COUNTRY: USA  
17 (F) ZIP: 77210-4433  
18  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
24  
25 (vi) CURRENT APPLICATION DATA:  
26 (A) APPLICATION NUMBER: 09/626,616  
27 (B) FILING DATE:  
28 (C) CLASSIFICATION:  
29  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: 08/305,518  
33 (B) FILING DATE:  
34  
35  
36 (viii) ATTORNEY/AGENT INFORMATION:  
37 (A) NAME: Wilson, Mark B.  
38 (B) REGISTRATION NUMBER: 37,259  
39 (C) REFERENCE/DOCKET NUMBER: INDA005\WIM  
40  
41 (ix) TELECOMMUNICATION INFORMATION:  
42 (A) TELEPHONE: 512-418-3000  
43 (B) TELEFAX: 512-474-7577  
44  
45  
46 (2) INFORMATION FOR SEQ ID NO:1:

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1618 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
53
54      (ii) MOLECULE TYPE: DNA (cdna)
55
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 214..1410
59
60
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63      CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG      60
64
65      CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA      120
66
67      GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC      180
68
69      AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA      234
70                      Met Asp Ser Ser Thr Gly Pro
71                      1          5
72
73      GGG AAC ACC AGC GAC TGC TCA GAC CCC TTA GCT CAG GCA AGT TGC TCC      282
74      Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser
75          10          15          20
76
77      CCA GCA CCT GGC TCC TGG CTC AAC TTG TCC CAC GTT GAT GGC AAC CAG      330
78      Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln
79          25          30          35
80
81      TCC GAT CCA TGC GGT CTG AAC CGC ACC GGG CTT GGC GGC AAC GAC AGC      378
82      Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser
83          40          45          50          55
84
85      CTG TGC CCT CAG ACC GGC AGC CCT TCC ATG GTC ACA GCC ATT ACC ATC      426
86      Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile
87          60          65          70
88
89      ATG GCC CTC TAC TCT ATC GTG TGT GTA GTG GGC CTC TTC GGA AAC TTC      474
90      Met Ala Leu Tyr Ser Ile Val Cys Val Val Gly Leu Phe Gly Asn Phe
91          75          80          85
92
93      CTG GTC ATG TAT GTG ATT GTA AGA TAC ACC AAA ATG AAG ACT GCC ACC      522
94      Leu Val Met Tyr Val Ile Val Arg Tyr Thr Lys Met Lys Thr Ala Thr
95          90          95          100
96
97      AAC ATC TAC ATT TTC AAC CTT GCT CTG GCA GAC GCC TTA GCG ACC AGT      570
98      Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Ala Thr Ser
99          105          110          115

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100																		
101	ACA	CTG	CCC	TTT	CAG	AGT	GTC	AAC	TAC	CTG	ATG	GGA	ACA	TGG	CCC	TTC		618
102	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe		
103	120					125					130					135		
104																		
105	GGA	ACC	ATC	CTC	TGC	AAG	ATC	GTG	ATC	TCA	ATA	GAT	TAC	TAC	AAC	ATG		666
106	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met		
107					140					145					150			
108																		
109	TTC	ACC	AGC	ATA	TTC	ACC	CTC	TGC	ACC	ATG	AGC	GTG	GAC	CGC	TAC	ATT		714
110	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile		
111				155					160					165				
112																		
113	GCT	GTC	TGC	CAC	CCA	GTC	AAA	GCC	CTG	GAT	TTC	CGT	ACC	CCC	CGA	AAT		762
114	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn		
115			170					175					180					
116																		
117	GCC	AAA	ATC	GTC	AAC	GTC	TGC	AAC	TGG	ATC	CTC	TCT	TCT	GCC	ATC	GGT		810
118	Ala	Lys	Ile	Val	Asn	Val	Cys	Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly		
119		185					190					195						
120																		
121	CTG	CCT	GTA	ATG	TTC	ATG	GCA	ACC	ACA	AAA	TAC	AGG	CAG	GGG	TCC	ATA		858
122	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile		
123	200					205					210					215		
124																		
125	GAT	TGC	ACC	CTC	ACG	TTC	TCC	CAC	CCA	ACC	TGG	TAC	TGG	GAG	AAC	CTG		906
126	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu		
127				220						225					230			
128																		
129	CTC	AAA	ATC	TGT	GTC	TTT	ATC	TTC	GCT	TTC	ATC	ATG	CCG	ATC	CTC	ATC		954
130	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala	Phe	Ile	Met	Pro	Ile	Leu	Ile		
131			235					240					245					
132																		
133	ATC	ACT	GTG	TGT	TAC	GGC	CTG	ATG	ATC	TTA	CGA	CTC	AAG	AGC	GTT	CGC		1002
134	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg		
135		250					255					260						
136																		
137	ATG	CTA	TCG	GGC	TCC	AAA	GAA	AAG	GAC	AGG	AAT	CTG	CGC	AGG	ATC	ACC		1050
138	Met	Leu	Ser	Gly	Ser</													

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153 AAC AGC TGC CTG AAT CCA GTT CTT TAC GCC TTC CTG GAT GAA AAC TTC      1242
154 Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
155          330                      335                      340
156
157 AAG CGA TGC TTC AGA GAG TTC TGC ATC CCA ACC TCG TCC ACG ATC GAA      1290
158 Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu
159          345                      350                      355
160
161 CAG CAA AAC TCC ACT CGA GTC CGT CAG AAC ACT AGG GAA CAT CCC TCC      1338
162 Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser
163          360                      365                      370                      375
164
165 ACG GCT AAT ACA GTG GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAG      1386
166 Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu
167          380                      385                      390
168
169 GCA GAA ACT GCT CCA TTG CCC TAACTGGGTC TCACACCATC CAGACCCTCG      1437
170 Ala Glu Thr Ala Pro Leu Pro
171          395
172
173 CTAAGCTTAG AGGCCGCCAT CTACGTGGAA TCAGGTTGCT GTCAGGGTGT GTGGGAGGCT      1497
174
175 CTGGTTTCCT GAGAAACCAT CTGATCCTGC ATTCAAAGTC ATTCCTCTCT GGCTACTTCA      1557
176
177 CTCTGCACAT GAGAGATGCT CAGACTGATC AAGACCAGAA GAAAGAAGAG ACTACCGGAC      1617
178
179 A      1618
180
181

```

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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193 Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro
194   1          5          10          15
195
196 Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu
197          20          25          30
198
199 Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr
200          35          40          45
201
202 Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser
203          50          55          60
204
205 Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val

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**RAW SEQUENCE LISTING**  
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206	65				70				75				80			
207																
208	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val	Arg	Tyr
209					85					90					95	
210																
211	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu
212				100					105					110		
213																
214	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr
215			115					120					125			
216																
217	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile
218		130					135					140				
219																
220	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr
221	145					150					155					160
222																
223	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu
224					165					170					175	
225																
226	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Val	Asn	Val	Cys	Asn	Trp
227				180					185					190		
228																
229	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr
230			195					200					205			
231																
232	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro
233		210					215					220				
234																
235	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala
236	225					230					235					240
237																
238	Phe	Ile	Met	Pro	Ile	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile
239					245					250					255	
240																
241	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu	Lys	Asp
242				260					265					270		
243																
244	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val	Ala	Val
245			275					280					285			
246																
247	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala
248		290					295					300				
249																
250	Leu	Ile	Thr	Ile	Pro	Glu	Thr									



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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/626,616**

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Line

Error

Original Text

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**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/09/626,616**

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*INPUT SET: S36161.raw*

< < THERE ARE NO ITEMS MISSING > >

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**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/09/626,616**

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*INPUT SET: S36161.raw*

Line	Original Text	Corrected Text
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